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Stubbs et al.

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(54) **CYTOCHROME C PROTEIN AND ASSAY**

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(30) **Foreign Application Priority Data**

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(51) **Int. Cl.**

G01N 33/00 (2006.01)

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C12N 1/20 (2006.01)

C07K 1/00 (2006.01)

(52) **U.S. Cl.** **436/86**; 435/252.3; 435/320.1;
530/350; 536/23.1

(58) **Field of Classification Search** 436/86;
536/23.1; 435/252.3, 320.1; 530/350
See application file for complete search history.

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Primary Examiner — Maryam Monshipouri

(57) **ABSTRACT**

The present invention relates to a cytochrome c-reporter
fusion protein construct comprising a modified cytochrome c
protein which targets the mitochondria and has a reduced
ability to induce apoptosis in a living cell. The invention also
relates to nucleic acid constructs encoding such protein
fusions and cells stably transfected with such constructs. The
stably transfected cells of the invention can be used in assays
to detect apoptosis.

29 Claims, 18 Drawing Sheets
(3 of 18 Drawing Sheet(s) Filed in Color)

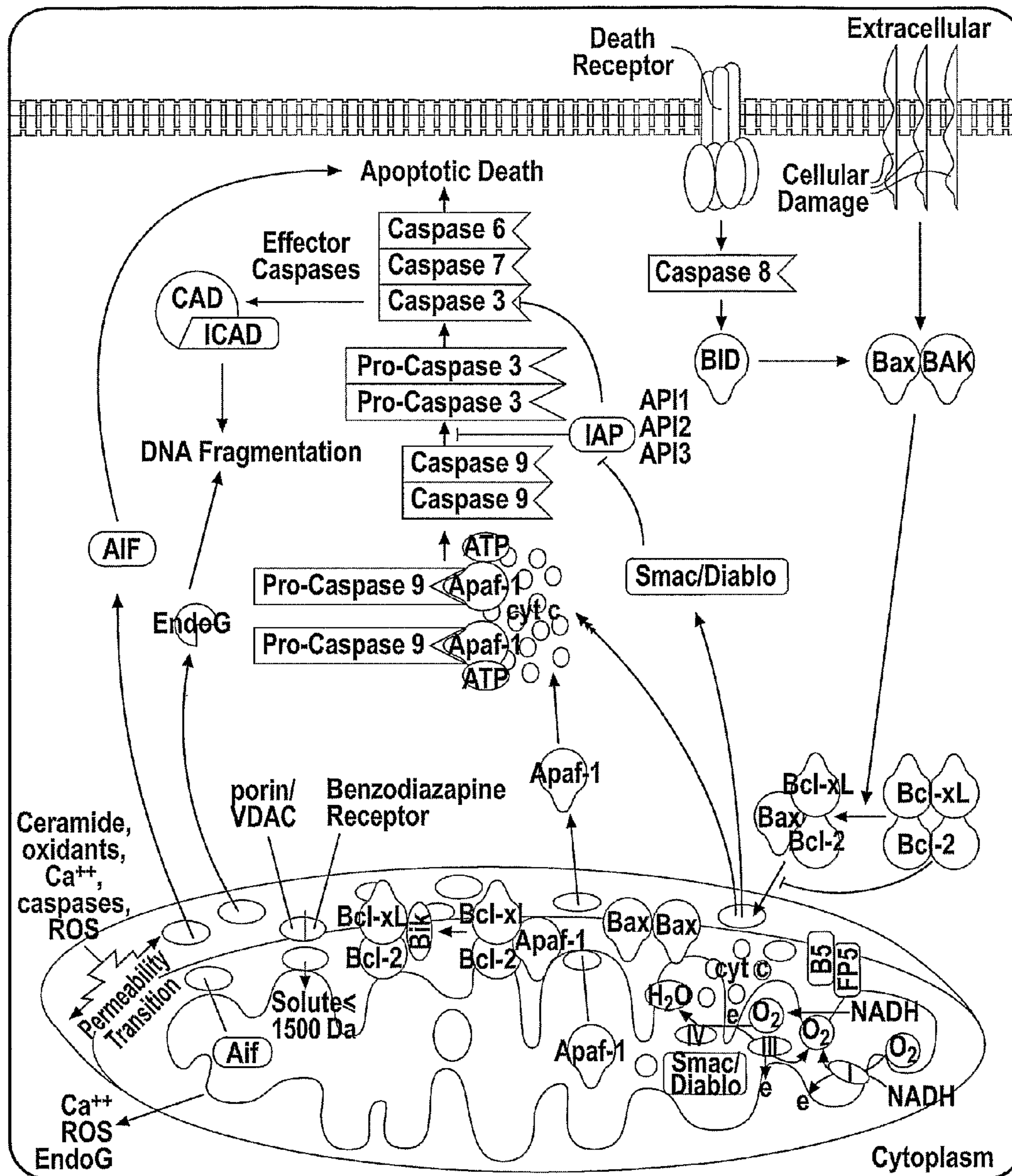


Fig. 1

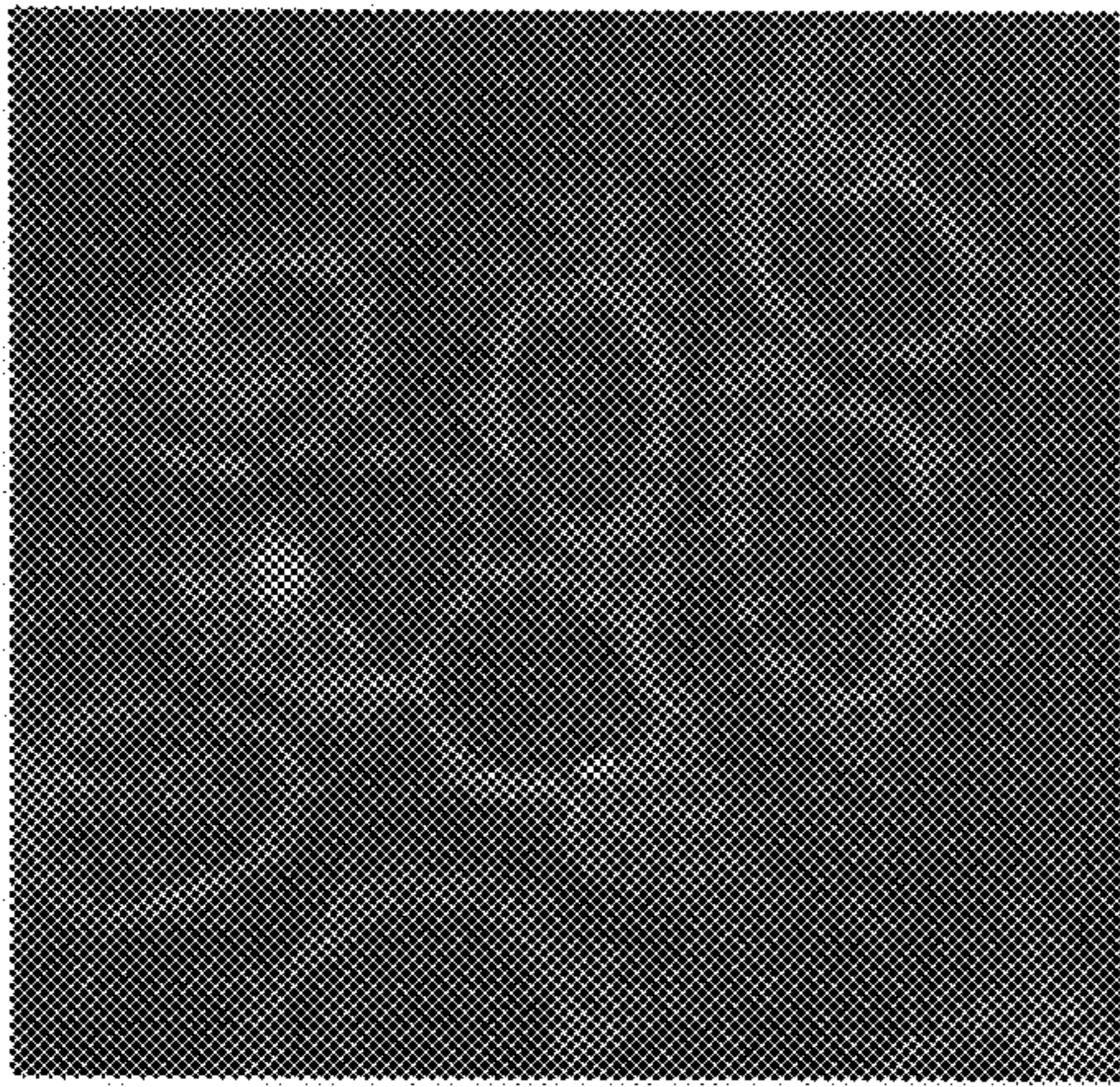


Figure 2a

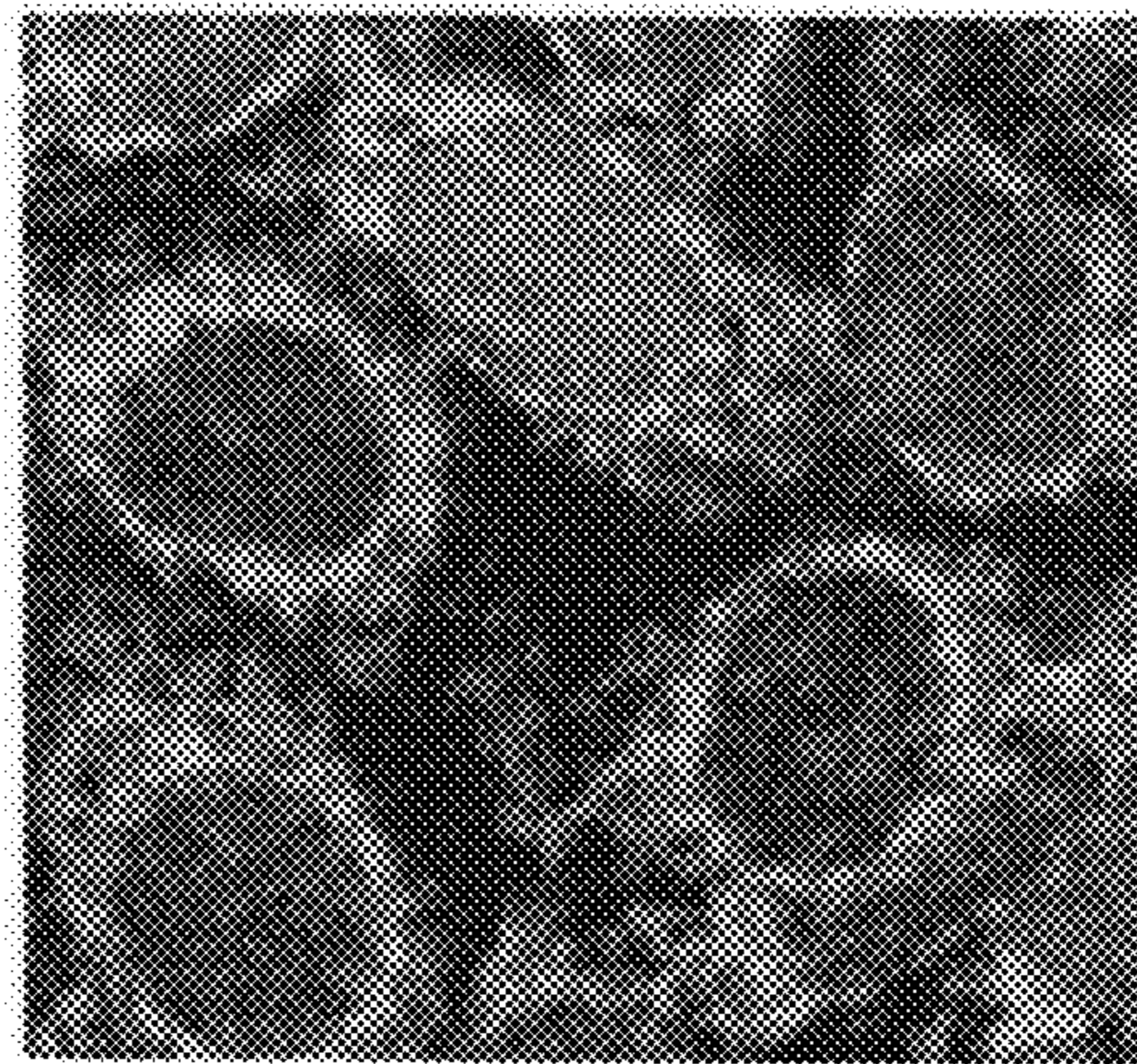


Figure 2b

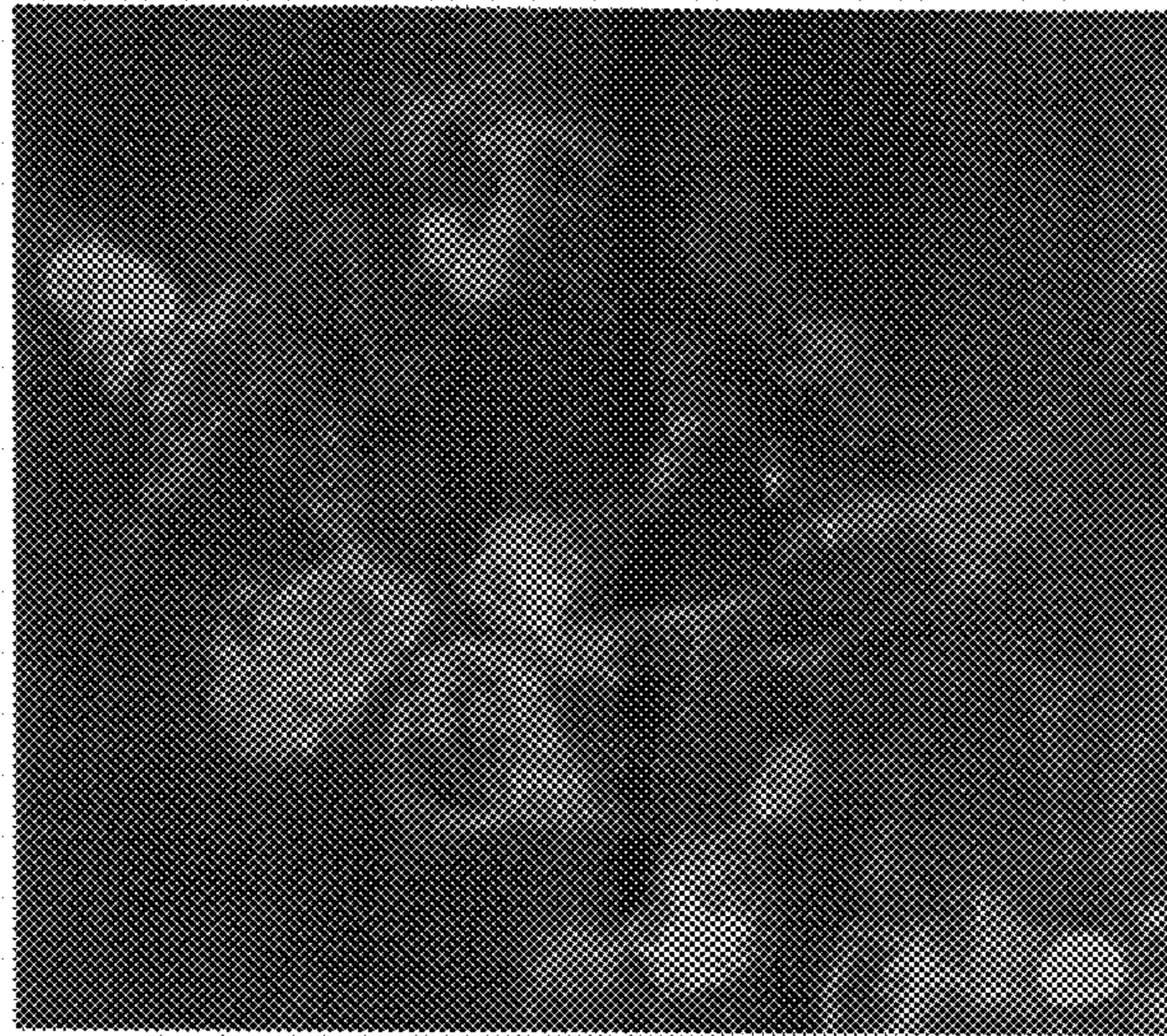


Figure 3a

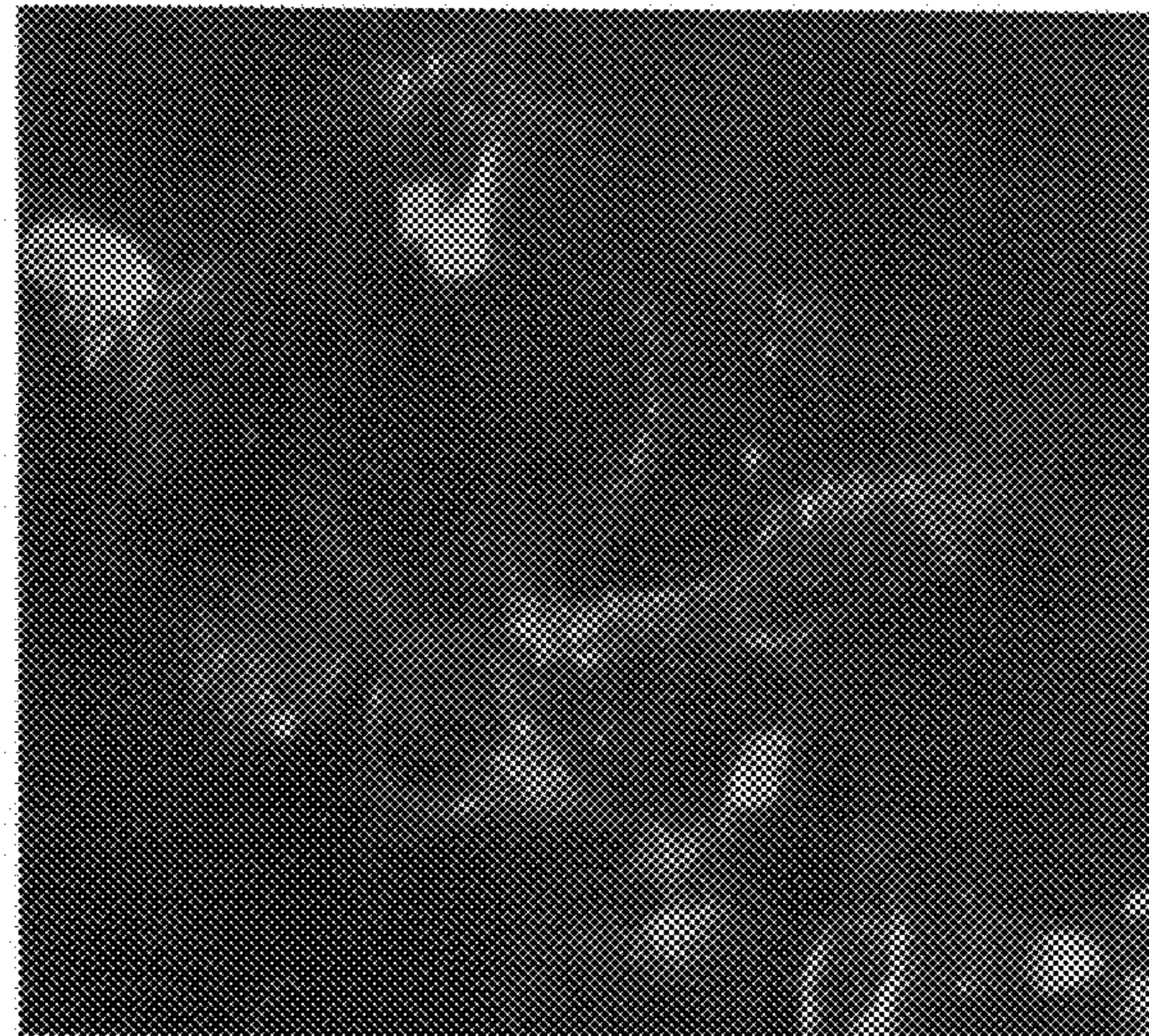


Figure 3b

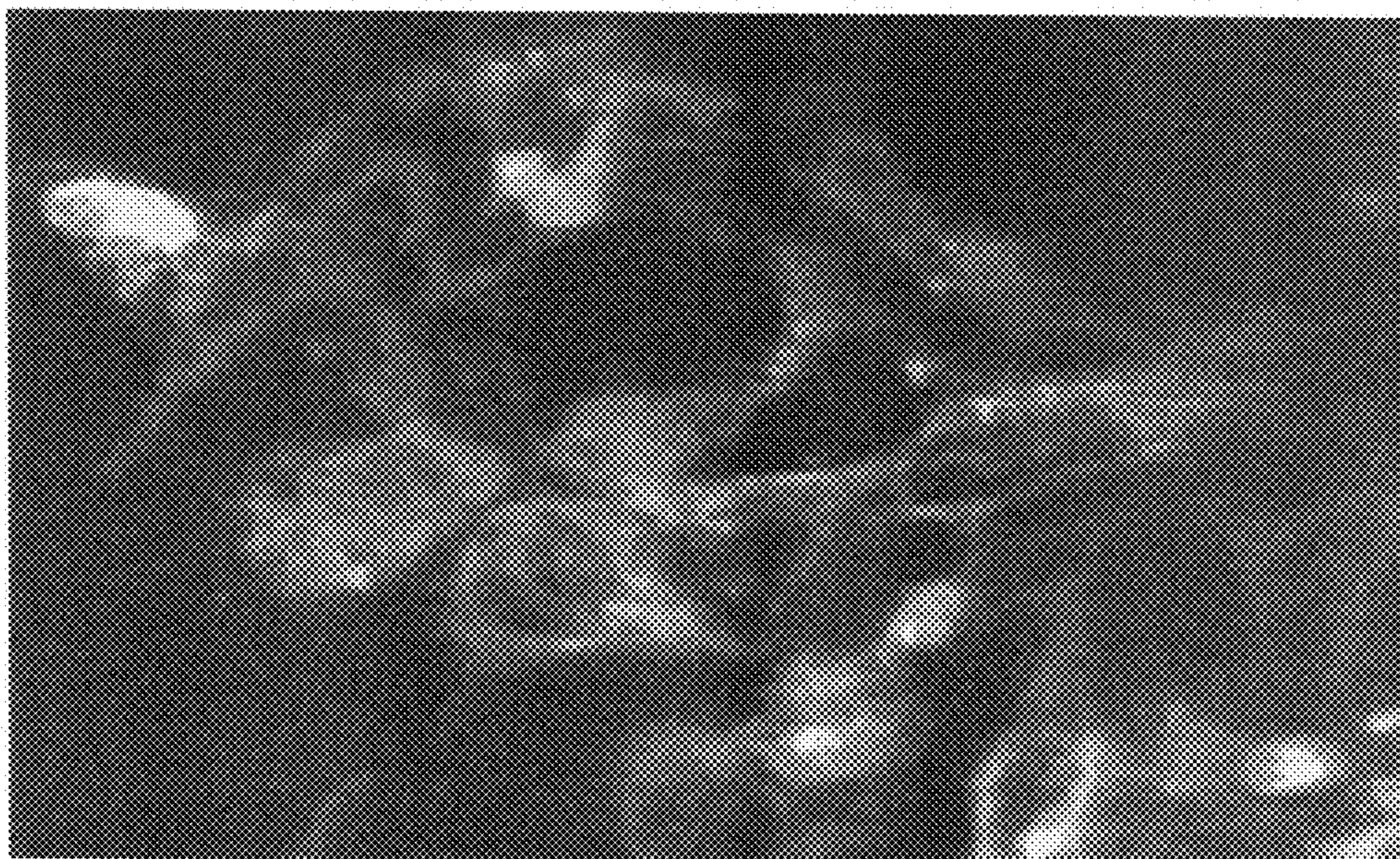


Figure 3c

Figure 4. SEQ ID NO: 1 - Wild Type Cytochrome C (NM_018947)

```
1   Met Gly Asp Val Glu Lys Gly Lys Lys Ile Phe Ile Met Lys Cys Ser
    ATG GGT GAT GTT GAG AAA GGC AAG AAG ATT TTT ATT ATG AAG TGT TCC

49   Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr Gly Pro Asn
    CAG TGC CAC ACC GTT GAA AAG GGA GGC AAG CAC AAG ACT GGG CCA AAT

97   Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro Gly Tyr Ser
    CTC CAT GGT CTC TTT GGG CGG AAG ACA GGT CAG GCC CCT GGA TAC TCT

145  Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly Glu Asp Thr
    TAC ACA GCC GCC AAT AAG AAC AAA GGC ATC ATC TGG GGA GAG GAT ACA

193  Leu Met Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile Pro Gly Thr Lys
    CTG ATG GAG TAT TTG GAG AAT CCC AAG AAG TAC ATC CCT GGA ACA AAA

241  Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala Asp Leu Ile
    ATG ATC TTT GTC GGC ATT AAG AAG AAG GAA GAA AGG GCA GAC TTA ATA

289  Ala Tyr Leu Lys Lys Ala Thr Asn Glu
    GCT TAT CTC AAA AAA GCT ACT AAT GAG
```

Figure 5. SEQ ID NO: 2 - Wild Type Cytochrome C (NM_018947)

1
Met Gly Asp Val Glu Lys Gly Lys Lys Ile Phe Ile Met Lys Cys Ser
17
Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr Gly Pro Asn
33
Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro Gly Tyr Ser
49
Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly Glu Asp Thr
65
Leu Met Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile Pro Gly Thr Lys
81
Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala Asp Leu Ile
97
Ala Tyr Leu Lys Lys Ala Thr Asn Glu

Figure 6. SEQ ID NO: 3 TriGFP-cytochrome C K72A

1	Met	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val
	ATG	AGT	AAA	GGA	GAA	GAA	CTT	TTC	ACT	GGA	GTT	GTC	CCA	ATT	CTT	GTT
49	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu
	GAA	TTA	GAT	GGT	GAT	GTT	AAT	GGG	CAC	AAA	TTT	TCT	GTC	AGT	GGA	GAG
97	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys
	GGT	GAA	GGT	GAT	GCA	ACA	TAC	GGA	AAA	CTT	ACC	CTT	AAA	TTT	ATT	TGC
145	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu
	ACT	ACT	GGA	AAA	CTA	CCT	GTT	CCA	TGG	CCA	ACA	CTT	GTC	ACT	ACT	CTC
193	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg
	TCT	TAT	GGT	GTT	CAA	TGC	TTT	TCA	AGA	TAC	CCA	GAT	CAT	ATG	AAA	CGG
241	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg
	CAT	GAC	TTT	TTC	AAG	AGT	GCC	ATG	CCC	GAA	GGT	TAT	GTA	CAG	GAA	AGA
289	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val
	ACT	ATA	TTT	TTC	AAA	GAT	GAC	GGG	AAC	TAC	AAG	ACA	CGT	GCT	GAA	GTC
337	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile
	AAG	TTT	GAA	GGT	GAT	ACC	CTT	GTT	AAT	AGA	ATC	GAG	TTA	AAA	GGT	ATT
385	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn
	GAT	TTT	AAA	GAA	GAT	GGA	AAC	ATT	CTT	GGA	CAC	AAA	TTG	GAA	TAC	AAC
433	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly
	TAT	AAC	TCA	CAC	AAT	GTA	TAC	ATC	ATG	GCA	GAC	AAA	CAA	AAG	AAT	GGA
481	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Gly	Val
	ATC	AAA	GTT	AAC	TTC	AAA	ATT	AGA	CAC	AAC	ATT	GAA	GAT	GGA	GGC	GTT
529	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro
	CAA	CTA	GCA	GAC	CAT	TAT	CAA	CAA	AAT	ACT	CCA	ATT	GGC	GAT	GGC	CCT
577	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser
	GTC	CTT	TTA	CCA	GAC	AAC	CAT	TAC	CTG	TCC	ACA	CAA	TCT	GCC	CTT	TCG
625	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Gly	Phe	Val
	AAA	GAT	CCC	AAC	GAA	AAG	AGA	GAC	CAC	ATG	GTC	CTT	CTT	GGC	TTT	GTA
673	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Leu	Glu
	ACA	GCT	GCT	GGG	ATT	ACA	CAT	GGC	ATG	GAT	GAA	CTA	TAC	AAA	CTC	GAG
721	Asn	Ser	Thr	Met	Gly	Asp	Val	Glu	Lys	Gly	Lys	Lys	Ile	Phe	Ile	Met
	AAT	TCG	ACC	ATG	GGT	GAT	GTT	GAG	AAA	GGC	AAG	AAG	ATT	TTT	ATT	ATG
769	Lys	Cys	Ser	Gln	Cys	His	Thr	Val	Glu	Lys	Gly	Gly	Lys	His	Lys	Thr
	AAG	TGT	TCC	CAG	TGC	CAC	ACC	GTT	GAA	AAG	GGA	GGC	AAG	CAC	AAG	ACT
817	Gly	Pro	Asn	Leu	His	Gly	Leu	Phe	Gly	Arg	Lys	Thr	Gly	Gln	Ala	Pro
	GGG	CCA	AAT	CTC	CAT	GGT	CTC	TTT	GGG	CGG	AAG	ACA	GGT	CAG	GCC	CCT
	Gly	Tyr	Ser	Tyr	Thr	Ala	Ala	Asn	Lys	Asn	Lys	Gly	Ile	Ile	Trp	Gly

Figure 6 (continued)

865 GGA TAC TCT TAC ACA GCC GCC AAT AAG AAC AAA GGC ATC ATC TGG GGA
Glu Asp Thr Leu Met Glu Tyr Leu Glu Asn Pro Ala Lys Tyr Ile Pro
913 GAG GAT ACA CTG ATG GAG TAT TTG GAG AAT CCC GCC AAG TAC ATC CCT
Gly Thr Lys Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala
961 GGA ACA AAA ATG ATC TTT GTC GGC ATT AAG AAG AAG GAA GAA AGG GCA
Asp Leu Ile Ala Tyr Leu Lys Lys Ala Thr Asn Glu
1009 GAC TTA ATA GCT TAT CTC AAA AAA GCT ACT AAT GAG

Figure 7: SEQ ID NO: 4 - triGFP-cytochrome C K72A

1
Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
17
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
33
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
49
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
65
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
81
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
97
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
113
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
129
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
145
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
161
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
177
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
193
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
209
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Gly Phe Val
225
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Leu Glu
241
Asn Ser Thr Met Gly Asp Val Glu Lys Gly Lys Lys Ile Phe Ile Met
257
Lys Cys Ser Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr
273
Gly Pro Asn Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro
289
Gly Tyr Ser Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly
305
Glu Asp Thr Leu Met Glu Tyr Leu Glu Asn Pro Ala Lys Tyr Ile Pro
321
Gly Thr Lys Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala
337
Asp Leu Ile Ala Tyr Leu Lys Lys Ala Thr Asn Glu

Figure 8. SEQ ID NO: 5 - Cytochrome C (K72A)-triGFP

Met Gly Asp Val Glu Lys Gly Lys Lys Ile Phe Ile Met Lys Cys Ser
1 ATG GGT GAT GTT GAG AAA GGC AAG AAG ATT TTT ATT ATG AAG TGT TCC

Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr Gly Pro Asn
49 CAG TGC CAC ACC GTT GAA AAG GGA GGC AAG CAC AAG ACT GGG CCA AAT

Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro Gly Tyr Ser
97 CTC CAT GGT CTC TTT GGG CGG AAG ACA GGT CAG GCC CCT GGA TAC TCT

Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly Glu Asp Thr
145 TAC ACA GCC GCC AAT AAG AAC AAA GGC ATC ATC TGG GGA GAG GAT ACA

Leu Met Glu Tyr Leu Glu Asn Pro Ala Lys Tyr Ile Pro Gly Thr Lys
193 CTG ATG GAG TAT TTG GAG AAT CCC GCC AAG TAC ATC CCT GGA ACA AAA

Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala Asp Leu Ile
241 ATG ATC TTT GTC GGC ATT AAG AAG AAG GAA GAA AGG GCA GAC TTA ATA

Ala Tyr Leu Lys Lys Ala Thr Asn Glu Gly Arg Pro Gly Met Ser Lys
289 GCT TAT CTC AAA AAA GCT ACT AAT GAG GGT CGA CCC GGG ATG AGT AAA

Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
337 GGA GAA GAA CTT TTC ACT GGA GTT GTC CCA ATT CTT GTT GAA TTA GAT

Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
385 GGT GAT GTT AAT GGG CAC AAA TTT TCT GTC AGT GGA GAG GGT GAA GGT

Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
433 GAT GCA ACA TAC GGA AAA CTT ACC CTT AAA TTT ATT TGC ACT ACT GGA

Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Ser Tyr Gly
481 AAA CTA CCT GTT CCA TGG CCA ACA CTT GTC ACT ACT CTC TCT TAT GGT

Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe
529 GTT CAA TGC TTT TCA AGA TAC CCA GAT CAT ATG AAA CGG CAT GAC TTT

Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
577 TTC AAG AGT GCC ATG CCC GAA GGT TAT GTA CAG GAA AGA ACT ATA TTT

Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
625 TTC AAA GAT GAC GGG AAC TAC AAG ACA CGT GCT GAA GTC AAG TTT GAA

Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
673 GGT GAT ACC CTT GTT AAT AGA ATC GAG TTA AAA GGT ATT GAT TTT AAA

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
721 GAA GAT GGA AAC ATT CTT GGA CAC AAA TTG GAA TAC AAC TAT AAC TCA

His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
769 CAC AAT GTA TAC ATC ATG GCA GAC AAA CAA AAG AAT GGA ATC AAA GTT

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala
817 AAC TTC AAA ATT AGA CAC AAC ATT GAA GAT GGA GGC GTT CAA CTA GCA

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu

Figure 8 (continued)

865 GAC CAT TAT CAA CAA AAT ACT CCA ATT GGC GAT GGC CCT GTC CTT TTA
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
913 CCA GAC AAC CAT TAC CTG TCC ACA CAA TCT GCC CTT TCG AAA GAT CCC
Asn Glu Lys Arg Asp His Met Val Leu Leu Gly Phe Val Thr Ala Ala
961 AAC GAA AAG AGA GAC CAC ATG GTC CTT CTT GGC TTT GTA ACA GCT GCT
Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
1009 GGG ATT ACA CAT GGC ATG GAT GAA CTA TAC AAA

Figure 9. SEQ ID NO: 6 - Cytochrome C (K72A)-triGFP

1
Met Gly Asp Val Glu Lys Gly Lys Lys Ile Phe Ile Met Lys Cys Ser
17
Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr Gly Pro Asn
33
Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro Gly Tyr Ser
49
Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly Glu Asp Thr
65
Leu Met Glu Tyr Leu Glu Asn Pro Ala Lys Tyr Ile Pro Gly Thr Lys
81
Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala Asp Leu Ile
97
Ala Tyr Leu Lys Lys Ala Thr Asn Glu Gly Arg Pro Gly Met Ser Lys
113
Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
129
Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
145
Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
161
Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Ser Tyr Gly
177
Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe
193
Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
209
Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
225
Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
241
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
257
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
273
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala
289
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
305
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
321
Asn Glu Lys Arg Asp His Met Val Leu Leu Gly Phe Val Thr Ala Ala
337
Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys

Figure 10. SEQ ID NO: 7 - TriGFP- wild type cytochrome C

1 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 ATG AGT AAA GGA GAA GAA CTT TTC ACT GGA GTT GTC CCA ATT CTT GTT
 49 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 GAA TTA GAT GGT GAT GTT AAT GGG CAC AAA TTT TCT GTC AGT GGA GAG
 97 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 GGT GAA GGT GAT GCA ACA TAC GGA AAA CTT ACC CTT AAA TTT ATT TGC
 145 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 ACT ACT GGA AAA CTA CCT GTT CCA TGG CCA ACA CTT GTC ACT ACT CTC
 193 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
 TCT TAT GGT GTT CAA TGC TTT TCA AGA TAC CCA GAT CAT ATG AAA CGG
 241 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 CAT GAC TTT TTC AAG AGT GCC ATG CCC GAA GGT TAT GTA CAG GAA AGA
 289 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 ACT ATA TTT TTC AAA GAT GAC GGG AAC TAC AAG ACA CGT GCT GAA GTC
 337 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 AAG TTT GAA GGT GAT ACC CTT GTT AAT AGA ATC GAG TTA AAA GGT ATT
 385 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 GAT TTT AAA GAA GAT GGA AAC ATT CTT GGA CAC AAA TTG GAA TAC AAC
 433 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 TAT AAC TCA CAC AAT GTA TAC ATC ATG GCA GAC AAA CAA AAG AAT GGA
 481 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
 ATC AAA GTT AAC TTC AAA ATT AGA CAC AAC ATT GAA GAT GGA GGC GTT
 529 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 CAA CTA GCA GAC CAT TAT CAA CAA AAT ACT CCA ATT GGC GAT GGC CCT
 577 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 GTC CTT TTA CCA GAC AAC CAT TAC CTG TCC ACA CAA TCT GCC CTT TCG
 625 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Gly Phe Val
 AAA GAT CCC AAC GAA AAG AGA GAC CAC ATG GTC CTT CTT GGC TTT GTA
 673 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Leu Glu
 ACA GCT GCT GGG ATT ACA CAT GGC ATG GAT GAA CTA TAC AAA CTC GAG
 721 Asn Ser Thr Met Gly Asp Val Glu Lys Gly Lys Lys Ile Phe Ile Met
 AAT TCG ACC ATG GGT GAT GTT GAG AAA GGC AAG AAG ATT TTT ATT ATG
 769 Lys Cys Ser Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr
 AAG TGT TCC CAG TGC CAC ACC GTT GAA AAG GGA GGC AAG CAC AAG ACT
 817 Gly Pro Asn Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro
 GGG CCA AAT CTC CAT GGT CTC TTT GGG CGG AAG ACA GGT CAG GCC CCT
 Gly Tyr Ser Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly

Figure 10 (continued)

865 GGA TAC TCT TAC ACA GCC GCC AAT AAG AAC AAA GGC ATC ATC TGG GGA
Glu Asp Thr Leu Met Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile Pro
913 GAG GAT ACA CTG ATG GAG TAT TTG GAG AAT CCC AAG AAG TAC ATC CCT
Gly Thr Lys Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala
961 GGA ACA AAA ATG ATC TTT GTC GGC ATT AAG AAG AAG GAA GAA AGG GCA
Asp Leu Ile Ala Tyr Leu Lys Lys Ala Thr Asn Glu
1009 GAC TTA ATA GCT TAT CTC AAA AAA GCT ACT AAT GAG

Figure 11. SEQ ID NO: 8 - TriGFP-wild type cytochrome C

1
Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
17
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
33
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
49
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
65
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
81
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
97
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
113
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
129
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
145
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
161
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
177
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
193
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
209
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Gly Phe Val
225
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Leu Glu
241
Asn Ser Thr Met Gly Asp Val Glu Lys Gly Lys Lys Ile Phe Ile Met
257
Lys Cys Ser Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr
273
Gly Pro Asn Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro
289
Gly Tyr Ser Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly
305
Glu Asp Thr Leu Met Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile Pro
321
Gly Thr Lys Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala
337
Asp Leu Ile Ala Tyr Leu Lys Lys Ala Thr Asn Glu

Figure 12. SEQ ID NO: 9 - Wild type Cytochrome C-triGFP

Met Gly Asp Val Glu Lys Gly Lys Lys Ile Phe Ile Met Lys Cys Ser
1 ATG GGT GAT GTT GAG AAA GGC AAG AAG ATT TTT ATT ATG AAG TGT TCC

Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr Gly Pro Asn
49 CAG TGC CAC ACC GTT GAA AAG GGA GGC AAG CAC AAG ACT GGG CCA AAT

Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro Gly Tyr Ser
97 CTC CAT GGT CTC TTT GGG CGG AAG ACA GGT CAG GCC CCT GGA TAC TCT

Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly Glu Asp Thr
145 TAC ACA GCC GCC AAT AAG AAC AAA GGC ATC ATC TGG GGA GAG GAT ACA

Leu Met Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile Pro Gly Thr Lys
193 CTG ATG GAG TAT TTG GAG AAT CCC AAG AAG TAC ATC CCT GGA ACA AAA

Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala Asp Leu Ile
241 ATG ATC TTT GTC GGC ATT AAG AAG AAG GAA GAA AGG GCA GAC TTA ATA

Ala Tyr Leu Lys Lys Ala Thr Asn Glu Gly Arg Pro Gly Met Ser Lys
289 GCT TAT CTC AAA AAA GCT ACT AAT GAG GGT CGA CCC GGG ATG AGT AAA

Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
337 GGA GAA GAA CTT TTC ACT GGA GTT GTC CCA ATT CTT GTT GAA TTA GAT

Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
385 GGT GAT GTT AAT GGG CAC AAA TTT TCT GTC AGT GGA GAG GGT GAA GGT

Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
433 GAT GCA ACA TAC GGA AAA CTT ACC CTT AAA TTT ATT TGC ACT ACT GGA

Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Ser Tyr Gly
481 AAA CTA CCT GTT CCA TGG CCA ACA CTT GTC ACT ACT CTC TCT TAT GGT

Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe
529 GTT CAA TGC TTT TCA AGA TAC CCA GAT CAT ATG AAA CGG CAT GAC TTT

Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
577 TTC AAG AGT GCC ATG CCC GAA GGT TAT GTA CAG GAA AGA ACT ATA TTT

Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
625 TTC AAA GAT GAC GGG AAC TAC AAG ACA CGT GCT GAA GTC AAG TTT GAA

Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
673 GGT GAT ACC CTT GTT AAT AGA ATC GAG TTA AAA GGT ATT GAT TTT AAA

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
721 GAA GAT GGA AAC ATT CTT GGA CAC AAA TTG GAA TAC AAC TAT AAC TCA

His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
769 CAC AAT GTA TAC ATC ATG GCA GAC AAA CAA AAG AAT GGA ATC AAA GTT

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala
817 AAC TTC AAA ATT AGA CAC AAC ATT GAA GAT GGA GGC GTT CAA CTA GCA

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu

Figure 12 (continued)

865 GAC CAT TAT CAA CAA AAT ACT CCA ATT GGC GAT GGC CCT GTC CTT TTA
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
913 CCA GAC AAC CAT TAC CTG TCC ACA CAA TCT GCC CTT TCG AAA GAT CCC
Asn Glu Lys Arg Asp His Met Val Leu Leu Gly Phe Val Thr Ala Ala
961 AAC GAA AAG AGA GAC CAC ATG GTC CTT CTT GGC TTT GTA ACA GCT GCT
Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
1009 GGG ATT ACA CAT GGC ATG GAT GAA CTA TAC AAA

Figure 13. SEQ ID NO: 10 - Wild Type Cytochrome C-triGFP

1
Met Gly Asp Val Glu Lys Gly Lys Lys Ile Phe Ile Met Lys Cys Ser
17
Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr Gly Pro Asn
33
Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro Gly Tyr Ser
49
Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly Glu Asp Thr
65
Leu Met Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile Pro Gly Thr Lys
81
Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala Asp Leu Ile
97
Ala Tyr Leu Lys Lys Ala Thr Asn Glu Gly Arg Pro Gly Met Ser Lys
113
Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
129
Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
145
Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
161
Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Ser Tyr Gly
177
Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe
193
Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
209
Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
225
Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
241
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
257
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
273
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala
289
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
305
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
321
Asn Glu Lys Arg Asp His Met Val Leu Leu Gly Phe Val Thr Ala Ala
337
Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys

CYTOCHROME C PROTEIN AND ASSAY

TECHNICAL FIELD

The present invention relates to a cytochrome c-reporter fusion protein construct which targets the mitochondria and has a reduced ability to induce apoptosis in a living cell. The fusion construct of the invention can be used in assays for detecting early events in apoptosis in living cells.

BACKGROUND TO THE INVENTION

'Programmed cell death' or apoptosis is a key event in multicellular organisms, defining a genetically encoded cell death program which is morphologically, biochemically and molecularly distinct from necrosis (Vermes et al., *J Immunol Meth.*, (2000) 243, 167-190). The characteristic morphological signs of apoptosis (cellular shrinkage, membrane blebbing, nuclear condensation and fragmentation) are the results of a complex biochemical cascade of events which is an integral part of physiological homeostasis.

Apoptosis ensures an equilibrium between cell proliferation and cell death, thus playing a regulatory role in the control of the size of cell populations and tissues. Aberrations in cell death signalling, in membrane or cytoplasmic receptors, or alterations in genes that govern apoptosis are involved in the pathogenesis of congenital malformations and many acquired diseases (Haanen & Vermes, *Eur J. Obstetr. Gynecol.*, (1996) 64, 129-133). Too little apoptosis may result in malignancies (Tomlinson & Bodmer, *Proc. Natl. Acad. Sci. USA*, (1995) 92, 11130-11134), Leukemias (Sachs, *Proc. Natl. Acad. Sci. USA*, (1996) 93, 4742-4749) or the resistance to anticancer therapy (Pahor et al., *Lancet*, (1996) 348, 493-497). Too much apoptosis can result in immune deficiency (Meyaard et al., *Science* (1992) 257, 217-219) and degenerative conditions (Griffith et al., *Science*, (1995) 270, 1189-1192).

There is therefore considerable interest within the medical, pharmaceutical and toxicological sciences in developing a greater understanding of the events which trigger and regulate apoptosis. Furthermore, there is a need to develop new techniques which can be used to identify, quantify and characterise agents which can modulate this phenomenon.

Assays for Detecting Apoptosis

A large number of assays have been developed to detect the onset of programmed cell death (Sgone & Wick, *Int Arch Allergy Immunol.*, (1994) 105, 327-332; Sgone & Gruber, *Exp Gerontol.*, (1998) 33, 525-533). These assays are based upon a wide range of events associated with cell death and have traditionally included light and electron microscopy with vital staining and nuclear dyes. Biochemical methods are often employed, for example based upon DNA laddering or degradation, DNA end labelling techniques (e.g. TUNEL—terminal deoxynucleotide transferase dUTP Nick End labelling), nuclease activity and lactate dehydrogenase enzyme release.

Flow cytometry tends to be the most widely used method (Vermes et al., *J Immunol Methods*, (2000) 243, 167-190) for detecting and quantifying apoptosis because it is amenable to screening large numbers of cells. This fluorescence-based technique employs vital dyes, antibodies to apoptotic enzymes (e.g. caspases) and single stranded DNA breaks, together with probes for measuring calcium flux and phospholipid redistribution.

Flow cytometry allows in vivo analysis of cells in suspension, one at a time, at rates of 1000 to 10,000 cells/s. However, one problem with flow cytometry is that it can only be used in

cells in suspension, such as liquid cell cultures and cells derived from the hemopoietic system. Furthermore flow cytometry of tissue cells requires physical and enzymatic manipulation to get the cells in suspension, which by itself may trigger apoptosis, necessitating checks by conventional light or fluorescence microscopy.

Existing methods are thus based upon late events in apoptosis (e.g. DNA degradation, caspase assays) and many require cellular fixation and staining with specific antibodies/dyes. None of the techniques described above provide a homogeneous living cell assay, based upon the early events in apoptosis, in real time nor discriminate from cellular necrosis. Furthermore, none of these assays are amenable to high throughput live cell screening which is required to test large numbers of compounds for their ability to modulate apoptosis.

Cytochrome c Translocation as a Marker for Apoptosis

Cytochrome c is a nuclear encoded protein which is targeted to the mitochondria where it performs its biological function as an electron carrier. The translocation of cytochrome c from the mitochondria to the cytoplasm in response to apoptotic stimuli is an early and critical step in the commitment of the cell to undergo apoptosis (Li et al., *Cell* (1997) 91, 479-489). Cytochrome c binds strongly to apoptosis protease activation factor-1 (Apaf-1) in the cytosol (Zou et al., *Cell* (1997) 90, 405-413). In the presence of cofactors the resulting cytochrome c: Apaf-1 assembles into a multimeric 'apoptosome' that binds and activates a protease zymogen, procaspase-9 (Srinivasula et al., *Mol. Cell* (1998) 1, 949-957). This results in the activation of the 'caspase cascade' whereby many intracellular substrates are cleaved disabling important cellular processes and breaking down structural components of the cell (Slee et al., *J Cell. Biol.* (1999) 144, 281-292; Skulachev, *FEBS Lett.*, (1998) 423, 275-280). A schematic diagram illustrating the mitochondrial role in apoptosis is shown in FIG. 1.

Recent in vitro studies (Kluck et al., *J. Biol. Chem.*, (2000), 275, 16127-16133; Yu et al., *J. Biol. Chem.*, (2001), 276, 1304-13038) have identified the molecular determinants involved in the cytochrome c: Apaf-1 interaction. Horse cytochrome c has been shown to be highly homologous to human cytochrome c and can initiate caspase activation, whereas yeast cytochrome c did not measurably bind to Apaf-1 nor activate caspase (Yu et al., *J Biol Chem.*, (2001) 276, 13034-13038). These studies focussed on the key differences between horse and yeast cytochrome c and used site directed mutagenesis to generate mutant variants which were subsequently analysed with respect to their ability to activate caspase. The results from this in vitro work indicated that residue 7, 25, 39, 62-65 and 72 were critical amino acids for cytochrome c: Apaf-1 interaction. Notably the mutation K72A showed no detectable binding or caspase-9 activation. While the mutation of lysine 72 to alanine abolished the interaction between cytochrome c and Apaf1, respiratory function of cytochrome c was unaffected.

Although the authors demonstrated reduced binding to Apaf-1 and caspase-9 activation in vitro it is not known whether the cytochrome c mutant proteins would behave in a similar manner in living cells, targeting the mitochondria and not inducing apoptosis.

Recent reports by Abdullaev et al. (*Biochem J.* (2002) 362, 749-754), again based on in vitro experiments, indicate that the horse K72 mutants described by Yu et al. (*J Biol Chem.*, (2001) 276, 13034-13038) show the same level of caspase activation as the wild-type protein if present at 2-12 fold higher concentrations than the wild type protein. In contrast, the authors reported that a horse K4E cytochrome c mutant

was inactive in activating caspase and conclude that this mutant, rather than K72 mutants, would be a good candidate for in vivo knock-in studies on the role of cytochrome c in apoptosis.

Fluorescent Proteins

The use of Green Fluorescent Protein (GFP) derived from *Aequorea victoria* is now well known for research into many cellular and molecular-biological processes. Cytochrome c-GFP fusions have been used in studies on apoptosis. Thus Heiskanen et al. (J Biol Chem., (1999) 274, 5654-5658) expressed a cytochrome c-GFP fusion, based upon rat cytochrome c, in rat pheochromocytoma-6 (PC6) cells. Induction of apoptosis by staurosporine led to release of the fusion from the mitochondria which was accompanied by mitochondrial depolarisation.

Goldstein et al., (Nat Cell Bio., (2000) 2, 156-160) demonstrated mitochondrial localisation of a cytochrome c-GFP fusion, based upon human cytochrome c, over-expressed in HeLa cells. A range of apoptotic inducers were shown to cause rapid release of cytochrome c-GFP.

Other researchers have also used cells which have been transiently transfected to over-produce cytochrome c-GFP fusion proteins to investigate apoptosis. Thus Goa et al., (J. Cell Sci., (2001) 114, 2855-2862) monitored the dynamic redistribution of GFP-tagged cytochrome c and the morphological changes of mitochondria within living HeLa cells during UV-induced apoptosis. Similarly, Lim et al., (J Biomed Sci (2002); 9, 488-506) explored the biochemical basis of cytochrome c-GFP localisation by transiently transfecting COS-7 cells with various GFP constructs and determining sub-cellular distribution using fluorescence and immunochemical techniques.

Problem to be Addressed

There is a need to develop sensitive assays which are amenable to high throughput screening in living cells and which allow detection and analysis in real time of the early events in apoptosis.

While over-expression of cytochrome c in cells has been demonstrated, the resulting high levels of protein lead to apoptosis and cell death, necessitating the use of complex inducible/transient systems for studies involving up-regulation of cytochrome c levels (Chandra et al., J Biol Chem. (2002) 277, 50842-50854). To date, it has not been possible to generate stable cell lines over-expressing this protein which could be reliably used for screening purposes.

There is thus a need for a cytochrome c protein which, when coupled to a reporter group to form a fusion construct, can be expressed in cells to provide stable cell lines. The resulting construct can act as a biosensor within the cells for early events in the induction or repression of apoptosis. Stable cell lines overexpressing such constructs are suitable for high throughput screening purposes to identify agents which modulate apoptosis.

The present invention addresses this problem and provides a fusion construct which has no observable toxicity to cells and acts as a biosensor to permit the detection of early events in apoptosis in living cells. The stably transformed cells of the invention can still undergo apoptosis due to the presence of endogenous cytochrome c, thus allowing detection and determination of a second apoptotic signaling event whether up or downstream of the cytochrome c translocation.

SUMMARY OF THE INVENTION

In a first aspect of the present invention there is provided a cytochrome c-reporter fusion protein construct comprising a modified cytochrome c protein or any functional analogue

thereof derived from wild type cytochrome c, wherein the modified cytochrome c targets the mitochondria and has a reduced ability to induce apoptosis in a living cell.

A reporter is to be understood to be any group that is detectable due to its radioactive, fluorescent or luminescent properties or is localisable by a detectable moiety such as a labeled antibody or specific binding compound.

Preferably, the modified cytochrome c binds apoptosis protease activation factor-1 (Apaf-1) at least 10 times less than wild type cytochrome c. More preferably, the modified cytochrome c binds Apaf-1 at least 100 times less than wild type cytochrome c. Most preferably, the modified cytochrome c binds Apaf-1 at least 1000 times less than wild type cytochrome c.

Suitably, at least one of the amino acids of the modified cytochrome c at positions 4, 7, 8, 25, 39, 62, 63, 64, 65 and 72 has been mutated relative to the wild type cytochrome c.

Suitably, the modified cytochrome c has an amino substitution or substitutions selected from the group consisting of K4E, K72A, K72L, K72R, K72G, K72X, E62N, K7E-K8E, K25P-K39H, K7A-E62N-K25P, K7A-E62N-K39H, K7E-K8E-E62N, K7A-K25P-E62N, K7A-E62N-K25P-K39H, E62N-T63N-L64M-M65S, K7E-K8E-E62N-K25P-K39H, K7E-K8E-K25P-E62N-T63N-L64M-M65S, K7E-K8E-K39H-E62N-T63N-L64M-M65S and K7E-K8E-K25P-K39H-E62N-T63N-L64M-M65S.

Preferably, the modified cytochrome c comprises the amino acid substitution selected from the group consisting of K7E-K8E-E62N-K25P-K39H, K7E-K8E-K25P-E62N-T63N-L64M-M65S, K7E-K8E-K39H-E62N-T63N-L64M-M65S and K7E-K8E-K25P-K39H-E62N-T63N-L64M-M65S.

More preferably, the modified cytochrome c comprises the amino acid substitution selected from the group consisting of K72A, K72L, K72R, K72G and K72X, wherein X represents trimethylation. Most preferably, the modified cytochrome c comprises the amino acid substitution K72A or K72L.

Preferably, modified cytochrome c comprises the amino acid substitution K4E.

Suitably, the reporter is a fluorescent protein or a functional analogue thereof.

It will be understood by the person skilled in the art that a functional analogue of a fluorescent protein will include, but is not limited to, any detectable fluorescent protein fragment formed in a protein fragment complementation assay as described, for example, in U.S. Pat. Nos. 6,270,964, 6,428,951 and 6,294,330.

Preferably, the fluorescent protein of the present invention is a Green Fluorescent Protein (GFP) derived from *Aequorea victoria*, *Renilla reniformis* or other members of the class *Anthozoa* (Labas et al., Proc. Natl. Acad. Sci., (2002), 99, 4256-4261).

U.S. Pat. No. 6,172,188 describes variant GFPs wherein the amino acid in position 1 preceding the chromophore has been mutated to provide an increase in fluorescence intensity. These mutants result in a substantial increase in the intensity of fluorescence of GFP without shifting the excitation and emission maxima. F64L-GFP has been shown to yield an approximate 6-fold increase in fluorescence at 37° C. due to shorter chromophore maturation time.

One mutant, commonly termed Enhanced Green Fluorescent Protein (EGFP), contains the mutations F64L and S65T (Cormack, B. P. et al., Gene, (1996), 173, 33-38). EGFP has been optimised for expression in mammalian systems, having been constructed with preferred mammalian codons.

Suitably, the fluorescent protein is selected from the group consisting of Green Fluorescent Protein (GFP), Yellow Fluoro-

rescent Protein (YFP), Blue Fluorescent Protein (BFP), Cyan Fluorescent Protein (CFP), Red Fluorescent Protein (RFP), Enhanced Green Fluorescent Protein (EGFP) and Emerald. Preferably, the fluorescent protein is either EGFP or Emerald.

GB 2374868 describes GFP derivatives having a triple mutation at F64, S65/E222 and S175 which exhibit enhanced fluorescence relative to wild type GFP when expressed in non-homologous cells at temperatures above 30°C. and when excited at about 490 nm. Mutant GFPs produced using the method of the invention provide a means for detecting GFP reporters in mammalian cells at lower levels of expression and/or increased sensitivity relative to wild type GFP.

Preferably, the GFP of the present invention comprises

- i) an amino acid substitution at position F64L;
- ii) an amino acid substitution at position S175G; and
- iii) an amino acid substitution at position E222G.

In a preferred embodiment the fusion construct is either SEQ ID NO: 4 or SEQ ID NO: 6.

In one embodiment, the reporter is localisable by a detectable luminescent, fluorescent or radio-active moiety. Thus, for example, the reporter comprises an immunogenic motif and the detectable moiety may be a luminescent, fluorescent or radio-actively labeled antibody.

Suitably, the reporter comprises a FLAG™, HA, HIS, c-Myc, VSV-G, V5 or a HSV (Sigma-Aldrich) epitope which is localisable by specific labeled antibodies.

In another embodiment, the reporter comprises a cysteine-rich motif and the detectable moiety comprises a labeled biarsenical compound as described by Griffin et al., Science (1998), 281, 269-272) and in U.S. Pat. Nos. 6,054,271, 6,008,378 and 5,932,474.

In a second aspect of the present invention, there is provided a nucleotide sequence encoding a protein fusion construct as hereinbefore described.

Preferably the nucleotide sequence is SEQ ID NO: 3 or SEQ ID NO: 5.

In a third aspect of the present invention, there is provided a nucleic acid construct comprises a suitable control region and the nucleotide sequence as hereinbefore described, the sequence being under the control of the control region.

Suitably, the nucleic acid construct is under the control of a promoter selected from the group consisting of native cytochrome c promoter, mammalian constitutive promoter, mammalian regulatory promoter, human ubiquitin C promoter, viral promoter, SV40 promoter, CMV promoter, yeast promoter, filamentous fungal promoter and bacterial promoter.

Preferably, the promoter is the CMV or the SV40 promoter. More preferably, the promoter is the human ubiquitin C promoter.

In a fourth aspect of the present invention, there is provided a replicable vector comprising a nucleic acid construct as hereinbefore described.

Suitably, the vector is a plasmid vector as described by Makrides (Prot Expression & Purif. (1999) 17, 183-202).

Preferably the vector is a viral vector. Suitable viral vectors for use in the invention are described, for example, by Ng et al., Hum Gene Ther. (2000) 11, 693-699 and include cytomegalovirus, Herpes simplex virus, Epstein-Barr virus, Simian virus 40, Bovine papillomavirus, Adeno-associated virus, Adenovirus, Vaccinia virus and Baculovirus vector.

In a fifth aspect of the present invention, there is provided a host cell stably transformed with a nucleic acid construct as hereinbefore described.

In a sixth aspect of the present invention, there is provided a host cell transiently transformed with a nucleic acid construct as hereinbefore described.

Suitably, the host cell is selected from the group consisting of plant, insect, nematode, bird, fish and mammalian cell. Preferably the cell is a human cell. More preferably the human cell is selected from the group consisting of Hek, Hela, U2OS and MCF-7. Most preferably the cell is Hek cell line 293 (Hek293).

Suitably, the host cell is capable of expressing the fusion protein as hereinbefore described.

In a seventh aspect of the present invention, there is provided a method for detecting apoptosis in a living cell comprising the steps of

- i) culturing a cell transformed to over-express a fusion construct as hereinbefore described;
- ii) determining the localisation of the fusion construct within the cell with time;

wherein a change in localisation of the fusion construct within the cell is indicative of apoptosis.

In an eighth aspect of the present invention, there is provided a method for measuring the effect an agent has upon modulating apoptosis in a living cell comprising the steps of

- i) culturing a cell transformed to over-express a fusion construct as hereinbefore described;
- ii) determining the localisation of the construct within the cell;

wherein any difference in the localisation of the construct within the cell relative to control cells untreated with the agent is indicative of the effect the agent has upon modulating apoptosis.

In a ninth aspect of the present invention, there is provided a method for measuring the effect an agent has upon modulating apoptosis in a living cell comprising the steps of

- i) culturing a first cell and a second cell which both over-express a fusion construct as hereinbefore described;
- ii) treating the first cell with the agent and determining the localisation of the construct within the first cell;
- iii) determining the localisation of the construct within the second cell which has not been treated with the agent;

wherein any difference in the localisation of the construct within the first cell and second cell is indicative of the effect the agent has upon modulating apoptosis.

In a tenth aspect of the present invention, there is provided a method for measuring the effect an agent has upon modulating apoptosis in a living cell comprising the steps of

- i) culturing a cell transformed to over-express a fusion construct as hereinbefore described;
- ii) treating the cell with the agent and determining the localisation of the construct within the cell;
- iii) comparing the localisation of the construct in the presence of the agent with a known value for the localisation of the construct in the absence of the agent;

wherein any difference in the localisation of the construct within the cell in the presence of the agent and the known value in the absence of the agent is indicative of the effect the agent has upon modulating apoptosis.

Suitably, the known value according is stored on a database, such as an electronic or optical database.

Suitably, the localisation of the protein fusion is measured by its luminescence, fluorescence or radioactive properties.

The method of the invention is suitable for screening purposes to identify agents which induce or inhibit apoptosis.

In another embodiment of the method of the invention, the localisation of the fusion construct is determined on non-living, fixed cells. Thus, the living cells over-expressing the fusion construct are fixed at specific time points by conventional means and the location of the fusion protein detected

using a detectable moiety, such as a labeled antibody or specific binding chemical. In this way, the effect an agent has upon apoptosis can be determined by comparing localisation of the fusion construct in the presence and the absence of the agent. Alternatively, the effect that the agent has upon apoptosis can be determined by comparing localisation of the construct in the presence of the agent against a known value (for example, one stored on a database) for localisation in the absence of the agent.

Suitably, the agent is a chemical, physical or biological agent. Examples of chemical agents include inorganic and organic compounds, such as drugs, toxins, peptides, proteins and nucleic acids. Physical agents include electromagnetic radiation such as electrical, magnetic and light (UV, gamma, IR, visible) energy. Examples of typical biological agents include viruses, prions, bacteria and fungi which could infect a living cell and modulate apoptosis.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1. Schematic representation depicting the mitochondrial role in apoptosis; reproduced by kind permission of Biocarta: (www.biocarta.com/pathfiles/h_mitochondriaPathway.asp).

FIG. 2a) InCell Analyzer 3000 images (ca. 40× magnification) showing cytochrome c (K72A-GFP mutant) labeled mitochondria in Hek 293 cells of clone 2B6.

FIG. 2b) Confocal microscopic image (ca. 60×) cytochrome c-GFP expression in HeLa cells (from Goldstein et al., (Nat Cell Bio., (2000) 2, 156-160))

FIG. 3a)-c). InCell Analyzer 3000 images showing colocalisation of cytochrome c (K72A mutant)-GFP and Tetramethylrhodamine ethyl ester (TMRE) using dual excitation of cytochrome c and TMRE in Hek 293 cells.

FIG. 3a) Cytochrome c (K72A)-GFP

FIG. 3b) TMRE labeled mitochondria

FIG. 3c) overlay of FIGS. 3a) & 3b) following dual excitation

FIG. 4. Nucleic acid sequence encoding wild type cytochrome c (SEQ ID NO: 1)

FIG. 5. Amino acid sequence of wild type cytochrome c (SEQ ID NO: 2)

FIG. 6. Nucleic acid sequence encoding F64L-S175G-E222G-triGFP-cytochrome c (K72A) construct (SEQ ID NO: 3)

FIG. 7. Amino acid sequence of F64L-S175G-E222G-triGFP-cytochrome c (K72A) construct (SEQ ID NO: 4)

FIG. 8. Nucleic acid sequence encoding cytochrome c (K72A)-F64L-S175G-E222G-triGFP (SEQ ID NO: 5)

FIG. 9. Amino acid sequence of cytochrome c (K72A)-F64L-S175G-E222G-triGFP (SEQ ID NO: 6)

FIG. 10. Nucleic acid sequence encoding F64L-S175G-E222G-wild type cytochrome c construct (SEQ ID NO: 7)

FIG. 11. Amino acid sequence of F64L-S175G-E222G wild type cytochrome c construct (SEQ ID NO: 8)

FIG. 12. Nucleic acid sequence encoding wild type cytochrome c-F64L-S175G-E222G tri GFP (SEQ ID NO: 9)

FIG. 13. Amino acid sequence of wild type cytochrome c-F64L-S175G-E222G tri GFP (SEQ ID NO: 10)

The file of this patent contains at least one drawing executed in color. Copies of this patent with color drawing(s)

will be provided by the Patent and Trademark Office upon request and payment of the necessary fee.

SPECIFIC EXAMPLES

Example 1

Amplification of the cytochrome c gene, fusion to GFP (F64L-S175G-E222G) and introduction of the K72A (APAF-1 binding) mutation.

The fluorescent-cytochrome c mutant fusion proteins of the current invention were produced by joining, in frame, a sequence of the nucleic acid that encodes for the cytochrome c protein to a sequence of the nucleic acid that encodes for a fluorescent protein and then introducing the K72A (APAF-1 binding) mutation (Kluck et al., J Biol Chem., (2000) 275, 16127-16133) to the nucleic acid of the fusion construct. A preferred sequence of the human cytochrome c gene is described by Zang and Gerstein (Gene, (2003) 312, 61-72); NCBI Accession number NM_018947. (SEQ ID NO: 1) the encoded protein is shown in SEQ ID NO: 2. Alternative human cytochrome c sequences may be used. In addition, alternative sequences around the start and stop codons of the gene may be used to provide useful restriction enzyme sites for protein fusion. Where such alterations change the amino acid numbering relative to the reference sequence such numbering should be inferred by amino acid alignment with the reference sequence. Preferred sequences of the gene encoding the fluorescent protein include those derived from *Aequorea victoria* published by Chalfie et al, (Science, (1994) 263, 802-5), the GFP-F64L-S175G-E222G mutant (GB Patent 2374868), Emerald (*Aurora biosciences*), EGFP and related mutants (BD Clontech, Palo Alto, Calif.), and fluorescent proteins from species of *Anthaxoa*, for review see Labas et al, (PNAS, (2002) 99, 4256-4261).

The cytochrome c gene was amplified by RT-PCR from a mixed human cDNA library using primers CYCS1 and CYCS2 or CYCS1 and CYCS3 according to recognised protocols (Sambrook, J. et al (2001) Molecular Cloning—A Laboratory Manual, Cold Spring Harbor Laboratory Press).

(SEQ ID NO: 11)

CYCS1; 5'-gttgaattcgaccatgggtgatgttgagaaaggc

(SEQ ID NO: 12)

CYCS2; 5'-gttggtgctcgaccttactcattagtagcttttttgag

(SEQ ID NO: 13)

CYCS3; 5'-gttggtgctcgacctcattagtagcttttttgag

Primer CYCS1 exhibits homology to the 5' region of the cytochrome c gene and contains both a partial Kozak sequence (Kozak, Cell (1986), 44, 283) and an EcoRI restriction enzyme site. Primer CYCS2 exhibits homology to the 3' region of the cytochrome c gene and contains a stop codon and SalI restriction enzyme site. Primer CYCS3 exhibits homology to the 3' region of the cytochrome c gene and contains a SalI restriction enzyme site. The CYCS1-CYCS2 and CYCS1-CYCS3 RT-PCR products were cloned into the corresponding EcoRI and SalI sites of the GFP-fusion vectors pCORON1000-GFP-C1 and N1, respectively (Amersham Biosciences, Cardiff, UK) and verified by automated sequencing. These vectors contain a CMV promoter to effect the expression of the GFP fusion and an SV40 promoter to elicit expression of a neomycin resistance marker. The GFP within these vectors is red-shifted and contains the mutations F64L-S175G-E222G as described in GB 2374868.

Cytochrome c (K72A) mutants were generated with the QuikChange™ site-directed mutagenesis kit (Stratagene, La Jolla, Calif., USA) using primers CYCS4 and CYCS5.

(SEQ ID NO: 14)
CYCS4; 5'-ggagtatattggagaatccccgccaagtagcatccctggaacaa

(SEQ ID NO: 15)
CYCS5; 5'-ttgttccaggatgtacttggcgggattctccaaataactcc

After sequence verification the pCORON1000-GFP-wild type cytochrome c and K72A mutant fusion constructs were sub-cloned into the vector pCORON2100 using the restriction enzymes NheI and NotI. pCORON2100 contains a CMV promoter and an IRES element to drive bicistronic expression of the GFP-fusion protein and a neomycin resistance marker.

The nucleic acid and amino acid sequences of the GFP-cytochrome c constructs obtained are shown in FIGS. 6 to 13 (SEQ ID NOS: 3-10)

Example 2

Influence of cytochrome c-K72A (APAF-1 binding) mutation upon GFP-fusion protein stable cell line generation in mammalian cells.

Plasmid DNA to be used for transfection was prepared for all constructs using the HiSpeed plasmid purification kit (Qiagen, Westberg, NL). In addition to the constructs in example 1, pCORON1000-GFP and pCORON2100-GFP were used as selection controls. DNA was diluted to 100 ng. μl^{-1} in 18-Megohm water (Sigma, Dorset, UK) and 1 μg used for transfections. For 50-80% confluency on the day of transfection, Hek293 cells were plated at a density of 5×10^4 /well in 6-well plates and incubated overnight. A 1:3 (1 μg :3 μl) ratio of DNA to FuGene6 reagent (Roche Diagnostics, Basel, Switzerland) was used for each transient transfection reaction; 3 μl FuGene6 was added to 87 μl serum-free DMEM medium (Sigma) (containing penicillin/streptomycin, L-glutamine [Invitrogen, Carlsbad, Calif.]) and gently tapped to mix, then 10 μl (1 μg) construct DNA was added and again gently mixed. The FuGene6: DNA complex was incubated at room temperature for 40 minutes and added dropwise, with gentle mixing, directly to the cells without changing the medium. The plates were then gently swirled for even distribution. Cells were monitored for expression after 24 and 48 hours using a Nikon Eclipse TE200 epifluorescent microscope (Nikon, Melville, N.Y.). Cells were passed into 15 cm

diameter plates and after 24 hours placed under selection with geneticin (G418, 250 ng. μl^{-1} ; Sigma). The concentration of geneticin was increased incrementally to 500 ng. μl^{-1} over the following 5-7 days. Selection continued for around 10 days or until cells in the mock-transfected control plates had died. Cloning rings were then used to isolate surviving colonies and cells were expanded through 96-well, 24-well and 6-well plates. Where appropriate second and third rounds of clonal selection were applied.

After the first round of clonal selection surviving cells were visible for transfections containing pCORON1000-GFP, pCORON2100-GFP and the pCORON2100-GFP-N and -C cytochrome c (K72A) mutant plasmids. No surviving colonies were obtained from cells transfected with other plasmid constructs.

Results

Expression studies of this mutated cDNA were performed in pCORON2100 (Amersham Biosciences) in order to utilise the IRES element and facilitate the generation of stable cell lines. A "mixed population" stably expressing cell line under selection with geneticin G418 was continuously cultured for 3 weeks. 15 single clonal cell lines were then isolated.

Hek293 cells containing the pCORON2100-GFP-cytochrome c (K72A) mutants were shown to exhibit stable expression during continuous culture over a 4 month period. The mitochondrial localisation of the reporter fusion proteins was confirmed during this period by co-localisation with the known mitochondrial marker mitotracker red (Molecular Probes, Eugene, Oreg.) using a Microsystems LSM (Zeiss, Thornwood, N.Y.) and a high throughput laser scanning confocal microscope (INCell Analyzer 3000, Amersham Biosciences).

The expression results from one of these stable clones (2B6), using the InCell Analyzer 3000 (Amersham Biosciences, UK) laser scanning confocal imaging system, are shown below in FIG. 2. As can be seen from FIG. 2a the localisation pattern of expressed cytochrome c-GFP closely resembles that observed by Goldstein et al., (Nat Cell Bio., (2000) 2, 156-160), using a confocal microscope, reproduced in FIG. 2b. As expected, the fusion protein demonstrates nuclear exclusion and localises to mitochondria, the cytochrome c-GFP displaying a punctuate pattern of fluorescence (FIG. 2a).

FIGS. 3a and 3b show localisation of the fusion protein construct (a) and the mitochondrial stain TMRE (b) at a concentration of 40 nM in the mitochondria of Hek 293 cells. Dual excitation of the cytochrome c-GFP and TMRE in the InCell Analyzer demonstrates co-localisation (FIG. 3c).

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 15

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<211> LENGTH: 315

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

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ggtgaaaagg gaggcaagca caagactggg ccaaatctcc atggtctctt tgggcggaag 120

acaggtcagg cccttgata ctcttacaca gccgccaata agaacaaagg catcatctgg 180

ggagaggata cactgatgga gtatttggag aatcccaaga agtacatccc tggaaacaaaa 240

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aaagctacta atgag 315

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<210> SEQ ID NO 2
<211> LENGTH: 105
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 2

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1           5           10           15
Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr Gly Pro Asn
20           25           30
Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro Gly Tyr Ser
35           40           45
Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly Glu Asp Thr
50           55           60
Leu Met Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile Pro Gly Thr Lys
65           70           75           80
Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala Asp Leu Ile
85           90           95
Ala Tyr Leu Lys Lys Ala Thr Asn Glu
100           105

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<210> SEQ ID NO 3
<211> LENGTH: 1044
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

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<400> SEQUENCE: 3

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gatgttaatg ggcacaaatt ttctgtcagt ggagaggggtg aaggtgatgc aacatacggg 120
aaacttacc cttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt 180
gtcactactc tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg 240
catgactttt tcaagagtgc catgcccga ggttatgtac aggaaagaac tatatctttc 300
aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggtga tacccttgtt 360
aatagaatcg agttaaagg tattgatttt aaagaagatg gaaacattct tggacacaaa 420
ttggaataca actataactc acacaatgta tacatcatgg cagacaaaca aaagaatgga 480
atcaaagtta acttcaaaat tagacacaa c attgaagatg gaggcgttca actagcagac 540
cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac 600
ctgtccacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt 660
cttggctttg taacagctgc tgggattaca catggcatgg atgaactata caaactcgag 720
aattcgacca tgggtgatgt tgagaaaggc aagaagattt ttattatgaa gtgttcccag 780
tgccacaccg ttgaaaaggg aggcaagcac aagactgggc caaatctcca tggctctttt 840
gggcggaaga caggtcaggc ccctggatac tcttacacag ccgccaataa gaacaaaggc 900
atcatctggg gagaggatac actgatggag tatttggaga atcccgcaa gtacatccct 960
ggaacaaaaa tgatctttgt cggcattaag aagaaggaag aaagggcaga cttaatagct 1020
tatctcaaaa aagctactaa tgag 1044

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<210> SEQ ID NO 4
<211> LENGTH: 348
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polypeptide

<400> SEQUENCE: 4

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1          5          10          15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20          25          30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35          40          45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50          55          60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65          70          75          80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85          90          95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100         105         110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115         120         125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130         135         140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145         150         155         160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
165         170         175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180         185         190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195         200         205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Gly Phe Val
210         215         220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Leu Glu
225         230         235         240

Asn Ser Thr Met Gly Asp Val Glu Lys Gly Lys Lys Ile Phe Ile Met
245         250         255

Lys Cys Ser Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr
260         265         270

Gly Pro Asn Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro
275         280         285

Gly Tyr Ser Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly
290         295         300

Glu Asp Thr Leu Met Glu Tyr Leu Glu Asn Pro Ala Lys Tyr Ile Pro
305         310         315         320

Gly Thr Lys Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala
325         330         335

Asp Leu Ile Ala Tyr Leu Lys Lys Ala Thr Asn Glu
340         345

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<210> SEQ ID NO 5
<211> LENGTH: 1041
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 5

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gttgaaaagg gaggcaagca caagactggg ccaaactctcc atggctctctt tgggcggaag    120
acaggtcagg cccctggata ctcttacaca gccgccaata agaacaaagg catcatctgg    180
ggagaggata cactgatgga gtatttggag aatcccgcc agtacatccc tggaacaaaa    240
atgatctttg tcggcattaa gaagaaggaa gaaagggcag acttaatagc ttatctcaaa    300
aaagctacta atgagggtcg acccgggatg agtaaaggag aagaactttt cactggagtt    360
gtcccaattc ttgttgaatt agatgggatg gtaaatgggc acaaattttc tgtcagtgga    420
gaggtgaag gtgatgcaac atacggaaaa cttaccctta aatttatttg cactactgga    480
aaactacctg ttccatggcc aacacttgtc actactctct cttatggtgt tcaatgcttt    540
tcaagatacc cagatcatat gaaacggcat gactttttca agagtgccat gcccgagggt    600
tatgtacagg aaagaactat atttttcaaa gatgacggga actacaagac acgtgctgaa    660
gtcaagtttg aaggtgatac ccttgtaaat agaatcgagt taaaaggat tgattttaaa    720
gaagatggaa acattcttgg acacaaattg gaatacaact ataactcaca caatgtatac    780
atcatggcag acaacaaaaa gaatggaatc aaagttaact tcaaaattag acacaacatt    840
gaagatggag gcgttcaact agcagacat tatcaacaaa atactccaat tggcgatggc    900
cctgtccttt taccagacaa ccattacctg tccacacaat ctgcccttc gaaagatccc    960
aacgaaaaga gagaccacat ggtccttctt ggctttgtaa cagctgctgg gattacacat   1020
ggcatggatg aactatacaa a                                     1041

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<210> SEQ ID NO 6

<211> LENGTH: 347

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic polypeptide

<400> SEQUENCE: 6

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Met Gly Asp Val Glu Lys Gly Lys Lys Ile Phe Ile Met Lys Cys Ser
1          5          10          15
Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr Gly Pro Asn
20          25          30
Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro Gly Tyr Ser
35          40          45
Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly Glu Asp Thr
50          55          60
Leu Met Glu Tyr Leu Glu Asn Pro Ala Lys Tyr Ile Pro Gly Thr Lys
65          70          75          80
Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala Asp Leu Ile
85          90          95
Ala Tyr Leu Lys Lys Ala Thr Asn Glu Gly Arg Pro Gly Met Ser Lys
100         105         110
Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
115         120         125
Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
130         135         140
Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly

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145	150	155	160
Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Ser Tyr Gly	165	170	175
Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe	180	185	190
Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe	195	200	205
Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu	210	215	220
Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys	225	230	235
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser	245	250	255
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val	260	265	270
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala	275	280	285
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu	290	295	300
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro	305	310	315
Asn Glu Lys Arg Asp His Met Val Leu Leu Gly Phe Val Thr Ala Ala	325	330	335
Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys	340	345	

<210> SEQ ID NO 7

<211> LENGTH: 1044

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 7

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gatgttaatg ggcacaaatt ttctgtcagt ggagaggggtg aaggtgatgc aacatacggg      120
aaacttacc c ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt      180
gtcactactc tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg      240
catgactttt tcaagagtgc catgcccga ggttatgtac aggaaagaac tatatttttc      300
aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggatg tacccttggt      360
aatagaatcg agttaaaggg tattgatttt aaagaagatg gaaacattct tggacacaaa      420
ttggaataca actataactc acacaatgta tacatcatgg cagacaaaca aaagaatgga      480
atcaaagtta acttcaaaat tagacacaac attgaagatg gaggcgttca actagcagac      540
cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac      600
ctgtccacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt      660
cttggttttg taacagctgc tgggattaca catggcatgg atgaactata caaactcgag      720
aattcgacca tgggtgatgt tgagaaaggc aagaagatgt ttattatgaa gtgttcccag      780
tgccacaccg ttgaaaaggg aggcaagcac aagactgggc caaatctcca tgggtctctt      840
gggcggaaga caggtcaggc ccttgatac tttacacag ccgccaataa gaacaaaggc      900
atcatctggg gagaggatac actgatggag tatttggaga atcccaagaa gtacatcctt      960

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ggaacaaaaa tgatctttgt cggcattaag aagaaggaag aaagggcaga cttaatagct 1020
tatctcaaaa aagctactaa tgag 1044

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<210> SEQ ID NO 8
<211> LENGTH: 348
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polypeptide

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<400> SEQUENCE: 8

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Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1          5          10          15
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20          25          30
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35          40          45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50          55          60
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65          70          75          80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85          90          95
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100         105         110
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115         120         125
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130         135         140
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145         150         155         160
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
165         170         175
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180         185         190
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195         200         205
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Gly Phe Val
210         215         220
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Leu Glu
225         230         235         240
Asn Ser Thr Met Gly Asp Val Glu Lys Gly Lys Lys Ile Phe Ile Met
245         250         255
Lys Cys Ser Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr
260         265         270
Gly Pro Asn Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro
275         280         285
Gly Tyr Ser Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly
290         295         300
Glu Asp Thr Leu Met Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile Pro
305         310         315         320
Gly Thr Lys Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala
325         330         335
Asp Leu Ile Ala Tyr Leu Lys Lys Ala Thr Asn Glu
340         345

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<210> SEQ ID NO 9
 <211> LENGTH: 1041
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 9

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acaggtcagg cccctggata ctcttacaca gccccaata agaacaaagg catcatctgg    180
ggagaggata cactgatgga gtatttgagg aatccaaga agtacatccc tggaacaaaa    240
atgatctttg tcggcattaa gaagaaggaa gaaagggcag acttaatagc ttatctcaaa    300
aaagctacta atgagggtcg acccgggatg agtaaaggag aagaactttt cactggagtt    360
gtccaatc ttgttgaatt agatgggatg gtaaatgggc acaaattttc tgcagtgga    420
gaggtgaag gtgatgcaac atacggaaaa cttaccctta aatttatttg cactactgga    480
aaactacctg ttccatggcc aacacttgtc actactctct cttatggtgt tcaatgcttt    540
tcaagatacc cagatcatat gaaacggcat gactttttca agagtgccat gccgaaggt    600
tatgtacagg aaagaactat atttttcaaa gatgacggga actacaagac acgtgctgaa    660
gtcaagtttg aaggtgatac cttgtttaat agaatcgagt taaaaggat tgattttaaa    720
gaagatggaa acattcttgg acacaaattg gaatacaact ataactcaca caatgtatac    780
atcatggcag acaaacaaaa gaatggaatc aaagttaact tcaaaattag acacaacatt    840
gaagatggag gcgttcaact agcagacat tatcaacaaa atactccaat tggcgatggc    900
cctgtccttt taccagacaa ccattacctg tccacacaat ctgccctttc gaaagatccc    960
aacgaaaaga gagaccacat ggtccttctt ggctttgtaa cagctgctgg gattacacat   1020
ggcatggatg aactatacaa a                                     1041

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<210> SEQ ID NO 10
 <211> LENGTH: 347
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic polypeptide

<400> SEQUENCE: 10

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Met Gly Asp Val Glu Lys Gly Lys Lys Ile Phe Ile Met Lys Cys Ser
1           5           10           15

Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr Gly Pro Asn
          20           25           30

Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro Gly Tyr Ser
          35           40           45

Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly Glu Asp Thr
          50           55           60

Leu Met Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile Pro Gly Thr Lys
65           70           75           80

Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala Asp Leu Ile
          85           90           95

Ala Tyr Leu Lys Lys Ala Thr Asn Glu Gly Arg Pro Gly Met Ser Lys
          100          105          110

Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
          115          120          125

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-continued

Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
 130 135 140
 Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
 145 150 155 160
 Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Ser Tyr Gly
 165 170 175
 Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe
 180 185 190
 Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
 195 200 205
 Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
 210 215 220
 Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
 225 230 235 240
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
 245 250 255
 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
 260 265 270
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala
 275 280 285
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 290 295 300
 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
 305 310 315 320
 Asn Glu Lys Arg Asp His Met Val Leu Leu Gly Phe Val Thr Ala Ala
 325 330 335
 Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 340 345

<210> SEQ ID NO 11
 <211> LENGTH: 34
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide primer

<400> SEQUENCE: 11

gttgaattcg accatgggtg atggtgagaa aggc

34

<210> SEQ ID NO 12
 <211> LENGTH: 37
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide primer

<400> SEQUENCE: 12

gttggtgctg accttactca ttagtagctt ttttgag

37

<210> SEQ ID NO 13
 <211> LENGTH: 34
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide primer

<400> SEQUENCE: 13

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34

<210> SEQ ID NO 14

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<211> LENGTH: 41
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide primer

<400> SEQUENCE: 14

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41

<210> SEQ ID NO 15
 <211> LENGTH: 41
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide primer

<400> SEQUENCE: 15

ttgttccagg gatgtacttg ggggattct ccaaatactc c

41

The invention claimed is:

1. A cytochrome C-reporter fusion protein construct comprising:

(a) a modified cytochrome C protein derived from wild type human cytochrome C represented by SEQ ID NO: 2; and

(b) a fluorescent protein,

wherein said fusion protein targets the mitochondria and has a reduced ability to induce apoptosis in a living cell, and

wherein said modified cytochrome C comprises the amino acid substitution selected from the group consisting of K73A, K73L, K73R, K73G and K73X, wherein X represents trimethylation.

2. The fusion construct of claim 1, wherein said modified cytochrome C binds apoptosis protease activation factor-1 (Apaf-1) at least ten times less than wild type cytochrome C.

3. The fusion construct of claim 1, wherein said modified cytochrome C binds apoptosis protease activation factor-1 (Apaf-1) at least 100 times less than wild type cytochrome C.

4. The fusion construct of claim 1, wherein said modified cytochrome C binds apoptosis protease activation factor-1 (Apaf-1) at least 1000 times less than wild type cytochrome C.

5. The fusion construct of claim 1, wherein said fluorescent protein is selected from the group consisting of Green Fluorescent Protein (GFP), Yellow Fluorescent Protein (YFP), Blue Fluorescent Protein (BFP), Cyan Fluorescent Protein (CFP), Red Fluorescent Protein (RFP), Enhanced Green Fluorescent Protein (EGFP) and Emerald.

6. The fusion construct of claim 1, wherein said fluorescent protein is Enhanced Green Fluorescent Protein or Emerald.

7. The fusion construct of claim 5, wherein said GFP comprises:

- i) an amino acid substitution at position F64L;
- ii) an amino acid substitution at position S175G; and
- iii) an amino acid substitution at position E222G.

8. The fusion construct of claim 1 selected from the group consisting of SEQ ID NO: 4 and SEQ ID NO: 6.

9. A nucleotide sequence encoding the fusion construct of claim 1.

10. A nucleotide sequence selected from the group consisting of SEQ ID NO: 3 and SEQ ID NO 5.

11. A nucleic acid construct comprising a suitable control region and the nucleotide sequence of claim 9, said sequence being under the control of said control region.

12. The nucleic acid construct of claim 11 being under the control of a promoter selected from the group consisting of native cytochrome C promoter, mammalian constitutive promoter, mammalian regulatory promoter, human ubiquitin C promoter, viral promoter, SV40 promoter, CMV promoter, yeast promoter, filamentous fungal promoter and bacterial promoter.

13. The nucleic acid construct of claim 12, wherein said viral promoter is the CMV or the SV40 promoter.

14. The nucleic acid construct of claim 12, wherein the promoter is the human ubiquitin C promoter.

15. A replicable vector comprising the nucleic acid construct of claim 11.

16. The replicable vector of claim 15, wherein said vector is a plasmid vector.

17. The replicable vector of claim 15, wherein the vector is a viral vector.

18. The replicable vector of claim 17, wherein said viral vector is selected from the group consisting of cytomegalovirus, Herpes simplex virus, Epstein-Barr virus, Simian virus 40, Bovine papillomavirus, Adeno-associated virus, Adenovirus, Vaccinia virus and Baculovirus vector.

19. A host cell stably transformed with the nucleic acid construct of claim 11.

20. A host cell transiently transformed with the nucleic acid construct of claim 11.

21. The host cell of claim 19 selected from the group consisting of plant, insect, nematode, bird, fish and mammalian cell.

22. The host cell of claim 21, wherein said mammalian cell is a human cell.

23. The host cell of claim 22, wherein said human cell is selected from the group consisting of Hek, HeLa, U2OS and MCF-7.

24. The host cell of claim 23, wherein said Hek cell is Hek293.

25. The host cell of claim 19 capable of expressing the fusion protein of claim 1.

26. A method for detecting apoptosis in a living cell comprising the steps of:

- i) culturing a cell transformed to over-express the fusion construct of claim 1; and
- ii) determining the localisation of the fusion construct within the cell with time; wherein a change in localisation of the fusion construct within the cell is indicative of apoptosis.

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27. The method of claim **26**, wherein the localisation of said fusion construct is measured by its luminescence, fluorescence or radioactive properties.

28. The method of claim **26**, wherein the localisation of the protein fusion is determined following fixation of the cells.

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29. The method of claim **26**, where the agent is a chemical, physical or biological agent.

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